

A microscopic view of various bacteria and viruses, rendered in a monochromatic orange color. The bacteria are elongated, some with flagella, and the viruses are spherical with textured surfaces. They are scattered across the frame, creating a sense of depth and movement.

# Gain greater **insights** into microbial mysteries

Innovative microbial sequencing solutions



# Working together to make an impact in the microbial world

Today more than ever, next-generation sequencing (NGS) is empowering a new level of accuracy and speed in obtaining answers in microbial and infectious disease research. This proven sequencing approach greatly enhances research efforts and offers potential solutions to address One Health issues.\*

## A broader view, a brighter future

With Illumina technology and support, researchers around the world are rapidly sequencing the genomes of microbes and gaining insights into their behavior, interactions with their hosts and environments, evolution, and circulation within and throughout global populations.

Depending on the microbes of interest, sample type, and the kinds of questions you want answered, different NGS workflows and solutions can be used. The optimal workflow should be determined by what goals need to be achieved.

## Illumina NGS solutions are up for the challenge

**Single-genome, multipathogen, and discovery workflows** can support the full range of microbiology and infectious disease research applications.

Illumina offers powerful library preparation kits, sequencing systems, and corresponding analysis and reporting solutions that enable discoveries and provide insights for a better understanding of the microbes most relevant to your research.



### ADVANCE YOUR RESEARCH

Learn how the right suite of NGS tools can help you gain a more complete picture in your research

\*One Health: [cdc.gov/onehealth](https://cdc.gov/onehealth).





WORKFLOW APPLICATION

# Microbial discovery

NGS is a useful approach for unbiased analysis of a primary sample. Shotgun DNA or RNA sequencing enables analysis of the genetic material present in complex microbial communities, such as environmental samples (eg, wastewater), human microbiomes, and primary samples (eg, sputum, lower respiratory aspirates).

## Metagenomics and metatranscriptomics

### Illumina DNA Prep [↗](#)

Fast, flexible library prep for microbiome discovery research and surveillance

Run multiple sample types, input amounts, and methods starting from DNA or cDNA

Access fast library prep with a total turnaround time of ~3.5 hours

Apply the DRAGEN™ Metagenomics pipeline to perform taxonomic classification of reads and provide single-sample and aggregate reporting

### Illumina Stranded Total RNA Prep with Ribo-Zero™ Plus Microbiome [↗](#)

Fast, efficient library prep that provides robust depletion of undesirable host and panbacterial rRNA from complex microbial samples for microbiome analysis

Eliminate unwanted rRNA from bacteria in complex microbial samples for highly efficient metatranscriptomics research

Obtain reliable results with an optimized library preparation workflow

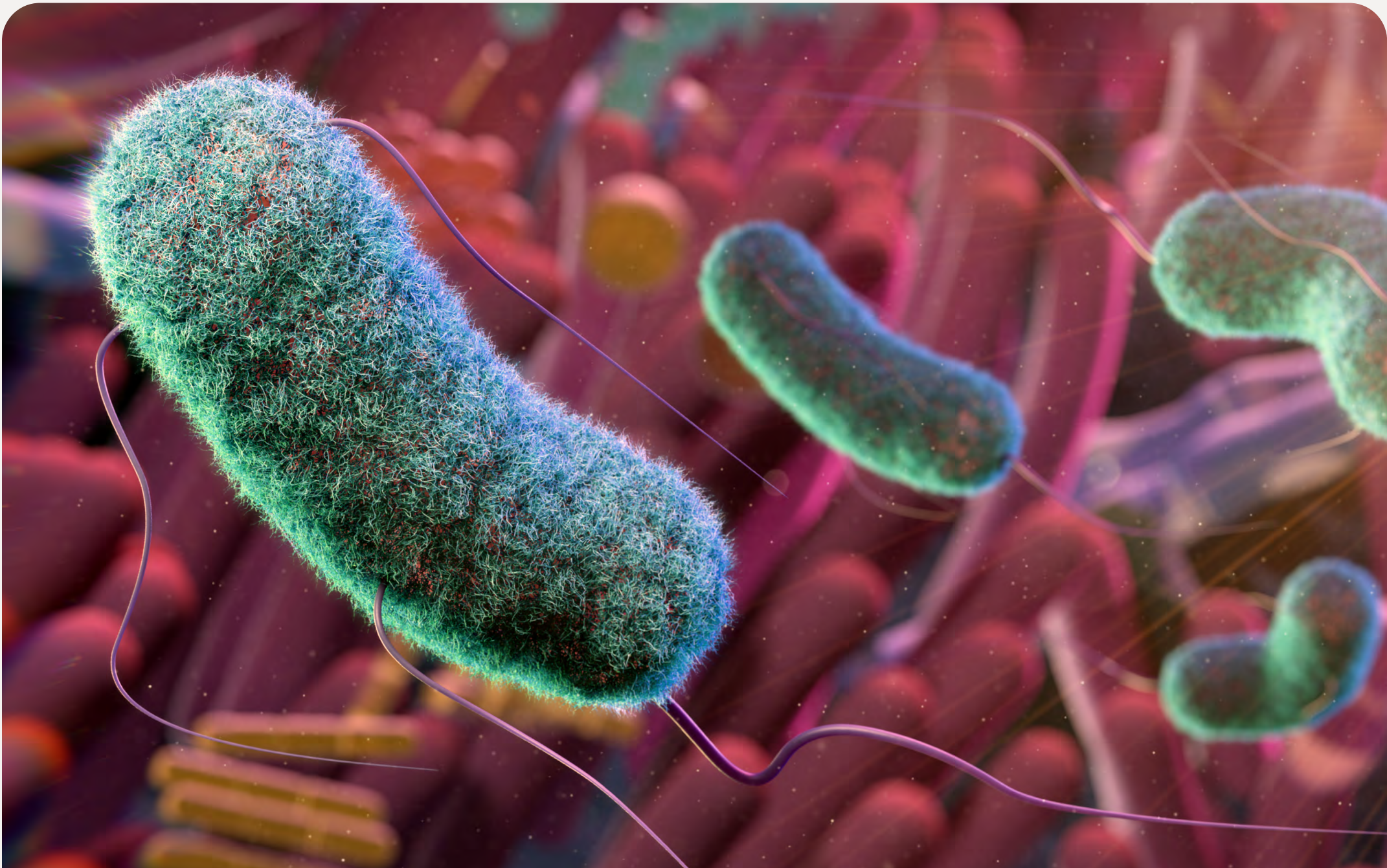
Simplify data analysis and visualization with the BaseSpace™ Microbiome Metatranscriptomics App



### UNCOVER MORE

Discover how metatranscriptomics enables community-level gene expression studies

Gut microbiome







## WORKFLOW APPLICATION

# Single-genome sequencing

Sequencing of a single pathogen is best used in situations when a single, known microbe is being analyzed.<sup>†</sup> These solutions will help you gain valuable insights in your research as you work to develop effective diagnostic tools, vaccines, and targeted therapies.



### MONITOR MORE

Download the single-genome sequencing methods guide to select the right solution for your lab

## Small whole-genome sequencing

### Illumina DNA Prep [↗](#)

Fast, flexible library preparation kit for characterizing cultured isolates; ideal for investigating foodborne outbreaks and health care–associated infections

Reduce library preparation time (~3.5 hours) with a low number of steps and minimal hands-on time

Obtain robust, consistent results over a wide range of DNA inputs, even at low amounts (1 ng)

## Targeted tuberculosis sequencing

### Illumina and GenoScreen Deeplex® Myc-TB Combo Kit [↗](#)

Determine tuberculosis (TB) strain and drug-resistance profiles faster than traditional culture-based methods for a more timely response to this critical public health threat

Produces results in < 48 hours directly from sputum, no culture required

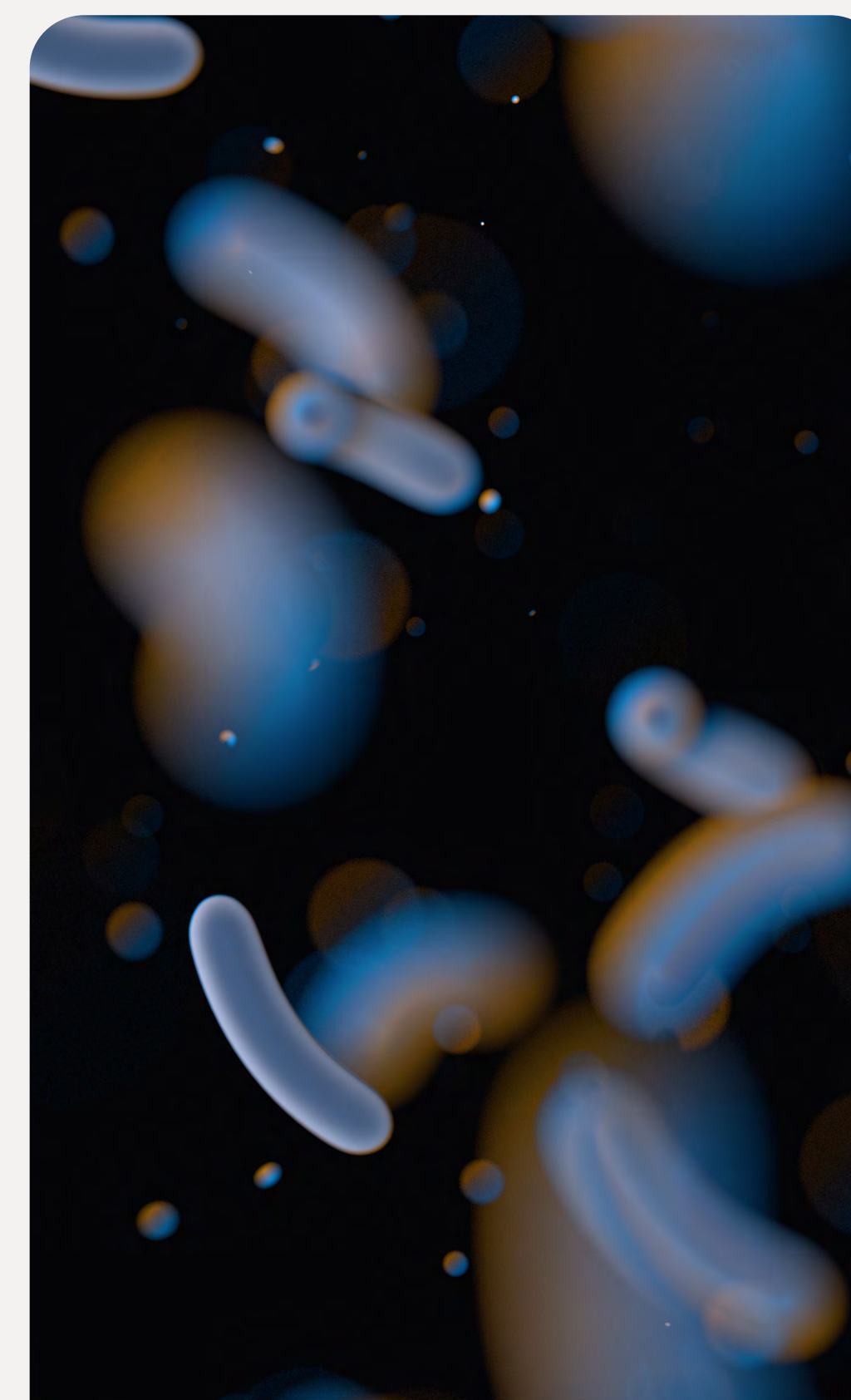
Predicts resistance to 15 anti-TB drugs

Provides secure, automated analysis and easy interpretation of results via the Deeplex Myc-TB Web App

*Mycobacterium tuberculosis* bacteria



*Escherichia coli* bacteria







# Single-genome sequencing

## Targeted virus characterization

### COVIDSeq™ Assay and COVIDSeq Test [↗](#)

Scalable, simple, and affordable solutions for whole-genome analysis of the SARS-CoV-2 virus to aid in COVID surveillance and viral research efforts

96- and 3072-sample kits available

Flexible input for multiple sample types, including nasal swabs and wastewater samples

Highly accurate virus characterization enabled by the DRAGEN Microbial Amplicon App

### Illumina Microbial Amplicon Prep–Influenza A/B [↗](#)

Simple and affordable whole-genome characterization of influenza A and B viruses for surveillance and seasonal vaccine research

Covers more than 98% of both influenza A and B virus genomes

Streamlines workflows; nine hours from extracted RNA to sequencing-ready library

Simplifies whole-genome analysis and variant interpretation with the DRAGEN Microbial Amplicon App

### Illumina Microbial Amplicon Prep [↗](#)

Flexible, streamlined NGS library preparation kit that enables various public health surveillance and microbial research applications

Pairs with lab-designed primers, published primers, or commercially available primer sets

Simplifies analysis with the DRAGEN Microbial Amplicon App

Enhances flexibility to accommodate different sample types, including nasal swabs, wastewater, and culture

*Influenza virus*







WORKFLOW APPLICATION

# Multipathogen sequencing

Hybrid-capture enrichment sequencing solutions are ideal when certain pathogens are suspected to be present or for surveillance of multiple known pathogens. They allow for targeted or whole-genome sequencing (WGS) of multiple organisms without requiring the high read depth needed for shotgun metagenomic sequencing of unenriched libraries.<sup>‡</sup>

## Broad viral, zoonotic, and environmental surveillance

### Viral Surveillance Panel v2 [↗](#)

Extensive WGS panel for reliable characterization of the most critical viral public health threats for broad-based surveillance efforts

Conduct WGS of > 200 viruses identified as high risk to public health and > 230 antiviral-resistance variants in influenza virus

Benefit from compatibility with a range of host and environmental sample types

Detect low-abundance viruses that shotgun sequencing would miss<sup>‡</sup>

Analyze and interpret data with ease using the DRAGEN Microbial Enrichment Plus App

### Respiratory Virus Enrichment Kit [↗](#)

Extensive, streamlined workflow offering highly sensitive detection and characterization of common respiratory viruses

Conduct WGS of > 40 respiratory viruses, including influenza A and B, SARS-CoV-2, and many more

Identify targeted viruses and new variants present and track variants from various sample types

Detect low-abundance viruses that shotgun sequencing would miss<sup>‡</sup>

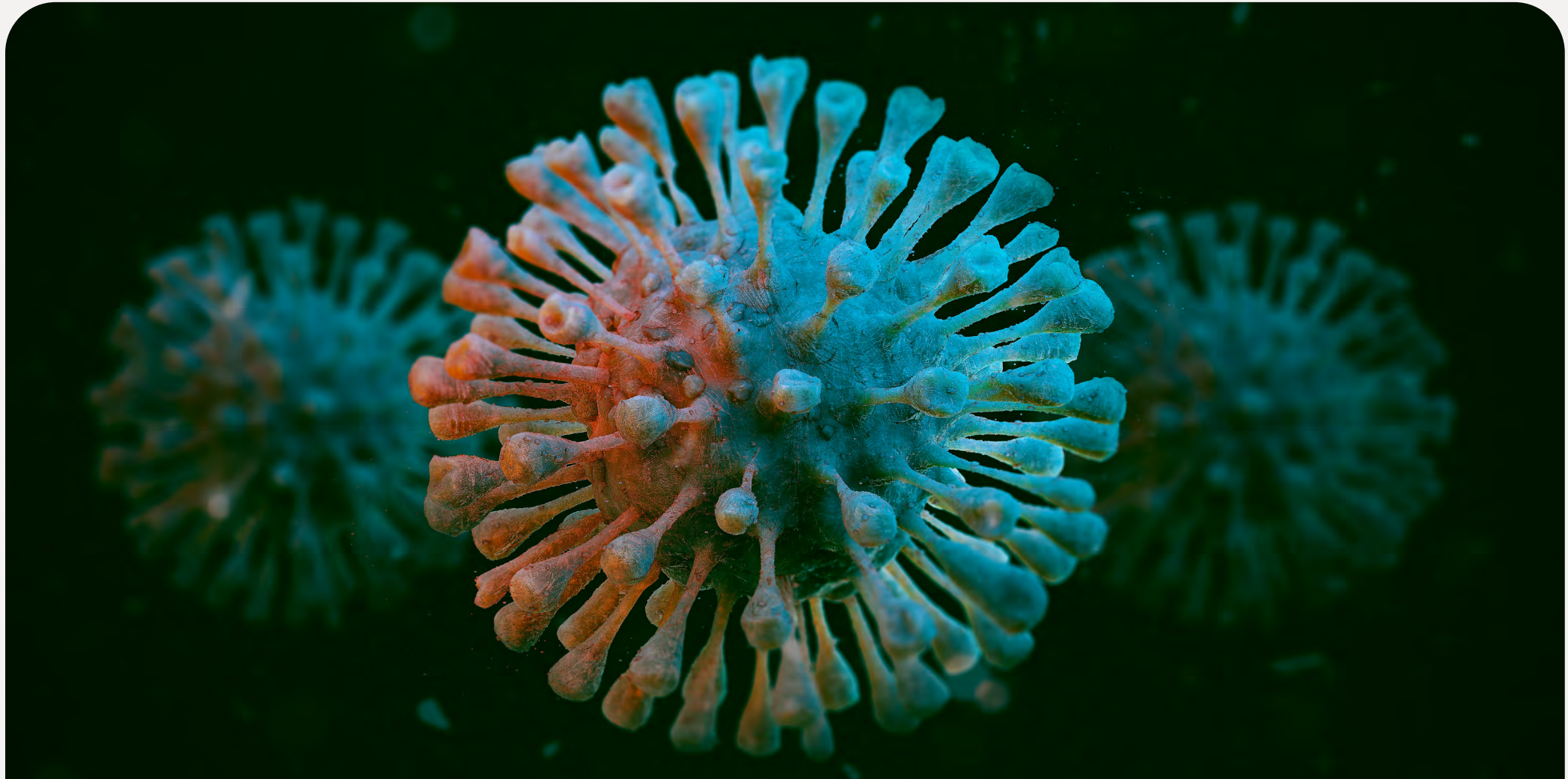
Analyze and interpret data with the DRAGEN Microbial Enrichment Plus App



### ANALYZE MORE

See how targeted microbial sequencing brings more profiling capabilities to your lab

Coronavirus (COVID-19)







# Multipathogen sequencing

## Flexible, comprehensive syndromic sequencing and antimicrobial resistance surveillance

### Respiratory Pathogen ID/AMR Enrichment Panel Kit [↗](#)

Comprehensive panel designed for reliable identification and quantification of respiratory pathogens and characterization of associated antimicrobial resistances for clinical research and surveillance

Identifies > 280 pathogens associated with respiratory tract infections

Characterizes antimicrobial resistance of > 2000 markers associated with 26 antimicrobial classes

Accommodates various sample types

Performs automated analysis powered by the DRAGEN Microbial Enrichment Plus App

### Urinary Pathogen ID/AMR Enrichment Panel Kit [↗](#)

The broadest sequencing-based panel for detecting urinary and sexually transmitted pathogens and their associated antimicrobial resistances for clinical research and surveillance

Identifies > 170 pathogens associated with urinary tract and sexually transmitted infections

Characterizes antimicrobial resistance of > 3700 markers associated with 18 antimicrobial classes

Accommodates various sample types

Performs automated analysis powered by the DRAGEN Microbial Enrichment Plus App



#### DETECT MORE

Download the Precision Metagenomics eBook to go deeper into sequencing possibilities

*Vibrio cholerae* bacteria





# Introducing the MiSeq™ i100 Series

## Impossibly simple sequencing, from setup to data analysis

The MiSeq i100 Series brings sequencing capabilities to users of all levels. Advancements in system design, sequencing chemistry, and data analysis integration deliver operational simplicity, exceptional speed, and proven accuracy.

As part of an end-to-end NGS solution, the MiSeq i100 Series provides same-day results for various applications that have impacts in infectious disease and microbiology. Whether tracking outbreaks, classifying novel microorganisms, or researching microbiomes, the simplicity of the MiSeq i100 Series enables sequencing with confidence and certainty.



### SIMPLIFIED RUN SET-UP

Completed in three steps in under 20 minutes. Download the MiSeq i100 Series infographic to learn more



### ENHANCED FLEXIBILITY

Multiple reagent kits support a wide range of throughputs and applications. Check out the MiSeq i100 Series virtual overview for details





## Scalable output enables expanded applications

With the MiSeq i100 Series, you can access 11 reagent configurations across multiple flow cell options and read lengths. You can readily increase sample throughput and perform deeper sequencing for various applications, from sWGS to metagenomics and more.

### MiSeq i100 System



MISEQ i100 SERIES

SEQUENCING SYSTEM

Outputs ranging from 1.5 to 25 Gb  
Read lengths from 1 × 100 bp to 2 × 500 bp  
5M and 25M flow cells

### MiSeq i100 Plus System



MISEQ i100 SERIES

PLUS

SEQUENCING SYSTEM


Outputs ranging from 1.5 to 30 Gb  
Read lengths from 1 × 100 bp to 2 × 500 bp  
5M, 25M, 50M, and 100M flow cells






# Choose the right platform for your lab

Trusted technology and proven performance empower microbiologists and infectious disease researchers to explore further, with confidence, so they can optimize its daily workflows.



EXPLORE MORE

Find additional details on Illumina sequencing platforms

			
Key specifications	MiSeq i100 Series	NextSeq™ 1000 and 2000 Systems	NovaSeq™ X Series
Max output per flow cell	30 Gb <sup>b</sup>	540 Gb <sup>a</sup>	8 Tb <sup>c</sup>
Run time (range)	~4–15 hr <sup>d</sup>	~8–44 hr <sup>d</sup>	~17–48 hr <sup>e</sup>
Max reads per run (single reads)	100M	1.8B <sup>a</sup>	26B (single flow cell) <sup>c</sup> 52B (dual flow cells) <sup>c</sup>
Max read length	2 × 500 bp	2 × 300 bp	2 × 150 bp
Ideal applications and methods <sup>f</sup>			
Small WGS	✓	✓	
Microbial community diversity analysis	✓	✓	
Shotgun metagenomics	✓	✓	✓
Microbial gene expression/ metatranscriptomics	✓	✓	✓
Microbial discovery	✓	✓	✓
Targeted pathogen surveillance	✓	✓	

a. Maximum specifications based on a P4 flow cell run; P4 flow cells are available for the NextSeq 2000 System only.

b. Maximum specifications based on a 100M flow cell run; 100M flow cells are available for the MiSeq i100 Plus System only.

c. Specifications based on the Illumina PhiX control library or a TruSeq™ DNA Library created with NA12878 at supported cluster densities. Performance may vary based on library type and quality, insert size, loading concentration, and other experimental factors.

d. Run times include cluster generation, sequencing, and base calling.

e. Run times include automated onboard cluster generation, sequencing, automated post-run wash, and base calling.

f. Check mark indicates an application or method optimized for the sequencing system.





## DATA ANALYSIS

# Turn data into meaningful results

Intuitive, efficient Illumina data analysis solutions are built with the same exceptional level of accuracy, accessibility, and security standards as Illumina sequencing solutions. The apps meet a broad range of microbial research, regardless of bioinformatics experience.



### EASY ACCESS

Explore BaseSpace Sequence Hub, a user-friendly genomics cloud-computing platform that helps simplify analysis

## Overview of apps

### Microbiome Metatranscriptomics App [↗](#)

Performs taxonomic and pathway enrichment analysis on metagenomic samples. Analyzes RNA sequencing libraries derived from microbiological communities using a four-step pipeline.

### 16S Metagenomics App [↗](#)

Analyzes DNA from amplicon sequencing of prokaryotic 16S small subunit rRNA genes. Provides visuals of taxonomic classification.

### SRST2 App [↗](#)

Reports the presence of STs (sequence types) from an MLST database and/or reference genes from a sequence data base of virulence genes, resistance genes, and plasmid replicons.

### Deeplex Myc-TB Web App\*\*

Provides secure, automated analysis and easy interpretation of results from the Illumina and GenoScreen Deeplex Myc-TB Combo Kit.

### DRAGEN small Whole Genome Sequencing (sWGS)

The DRAGEN sWGS App enables read mapping of single microbial genomes to a reference genome.

### DRAGEN Microbial Enrichment Plus App [↗](#)

Delivers easy-to-use, powerful secondary analysis of Illumina infectious disease and microbiology hybrid-capture enrichment panel kits, with workflows for sample QC, viral WGS, pathogen detection and quantification, and antimicrobial resistance (AMR) marker profiling.

### DRAGEN Metagenomics Pipeline [↗](#)

Aligns reads from shotgun metagenomic samples to genomic references, classifying to the lowest common level (down to genus level). Provides taxonomic classification for complex microbial samples.

### DRAGEN Microbial Amplicon App [↗](#)

Analyzes sequencing libraries generated from Illumina infectious disease and microbiology amplicon panel kits, such as the COVIDSeq Test and Illumina Microbial Amplicon Prep.





## Working as one, your lab and Illumina can bring the benefits of NGS-powered microbiology and infectious disease research to everyone

### How can we help you? [↗](#)

At Illumina, we offer technology and support to cover integrated NGS workflows—from library preparation to sequencing to data analysis to sharing. With optimized end-to-end solutions, you'll experience unrivaled accuracy, operational simplicity, and fast turnaround times.

### Illumina is committed to promoting global health [↗](#)

Beyond product offerings, Illumina offers a wide range of educational resources, support, and training programs to enhance your research. Let's make an impact, together.

### Learn how NGS can support your microbiology research goals [↗](#)

NGS is opening new doors in microbial genomics, revealing fresh insight into how microbes impact humans and the environment. With NGS, see the bigger picture by examining the smallest details in the tiniest organisms. Learn more about how NGS can change your approach to microbiology.

### Find the right workflow for your microbiology application [↗](#)

Take the guesswork out of your next workflow. The NGS Workflow Finder provides personalized solution recommendations and resources for your microbiology and infectious disease applications.



We are always available for questions, insights, and conversation.  
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